

Result No.	Score	Query	Match Length	DB ID	Description
1	470.6	B1174328_OSTF019E1	31	4	AV198059
c 2	374	B1175258_OSTR019E1	24	9	AV192017
c 3	362	C66636_C66636	24	1	C39939_C39939
c 4	361.4	C47805_C47805	24	1	Yuj1
5	360	AV190680	24	0	Yuj1
6	350.6	AV186436	23	4	Yuj1
					Copyright (c) 1993 - 2003 Compugen Ltd.
					GenCore version 5.1.6
					OM nucleic - nucleic search, using sw model
Run on:	July 15, 2003, 06:15:48	Search time 2313 Seconds (without alignments)			
Title:	US-09-043-944-5	1500	10502.910 Million cell updates/sec		
Perfect score:		1 gtttaattacccaatggttga.....taaaaaaaaaaaaaaa 1500			
Sequence:					
Scoring table:	IDENTITY_NUC				
	Gapoff 10.0 , Gapext 1.0				
Searched:	16154066 seqs, 8097743376 residues				
Total number of hits satisfying chosen parameters:	32308132				
Minimum DB seq length: 0					
Maximum DB seq length: 20000000000					
Post-processing: Minimum Match 0%					
Maximum Match 100%					
Listing first 75 summaries					
Database :	ESTB.*				
	1: em_estba.*				
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	10: gb_est2.*				
	11: gb_htc.*				
	12: gb_est3.*				
	13: gb_est4.*				
	14: gb_est5.*				
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	16: em_estom.*				
	17: gb_gss.*				
	18: em_gss_hum.*				
	19: em_gss_inv.*				
	20: em_gss_pln.*				
	21: em_gss_vt.*				
	22: em_gss_fun.*				
	23: em_gss_mam.*				
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	25: em_gss_other.*				
	26: em_gss_pro.*				
	27: em_gss_rnd.*				
					Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
					SUMMARIES
					8
Result No.	Score	Query	Match Length	DB ID	

RESULT	1	241	TGTCACGGAAACAGACAGTATCGTGAGAGGGATTGATGTCATGGRAATGCTCTCG	300
LOCUS	BI174328	477 bp	mRNA linear	EST 09-JUL-2001
DEFINITION	AD-wrmCDNA Caenorhabditis elegans cDNA similar to AD50991, mRNA sequence.			
ACCESSION	BI174328			
VERSION	BI174328-1			
KEYWORDS	GT:14640131			
SOURCE	Caenorhabditis elegans			
ORGANISM	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peleodinae; Caenorhabditis.			
REFERENCE	Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T., Jackson,C., Shin,I.T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J., Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F., Brasch,M.A., Vandenevoorde,J., Lamesch,P.E., Hill,D.E., and Vidal,M.	RESULT 2		
AUTHORS	Open reading-frame sequence tags (OSTS) support the existence of at least 17,300 genes in C. elegans	LOCUS	BI175258	386 bp mRNA linear EST 09-JUL-2001
TITLE	Nat. Genet. 27 (3), 332-336 (2001)	DEFINITION	OSTR019E11_1 AD-wrmCDNA Caenorhabditis elegans cDNA similar to AAD50991, mRNA sequence.	
JOURNAL		ACCESSION	BI175258	
MEDLINE		VERSION	BI175258.1	GI:14641061
COMMENT	Contact: Reboul J, Vaglio P	EST.		
	Marc Vidal Laboratory	ORGANISM	Caenorhabditis elegans	
	Dana Farber Cancer Institute		Caenorhabditis elegans	
	44 Binney Street, Boston, MA 02115, USA		Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditidae	
	TeL: 617 632 5180		; Rhabditidae; Peloderaeina; Caenorhabditis.	
	Fax: 617 632 2425		1 (bases 1 to 386)	
	Email: Jerome.Reboul@dfci.harvard.edu	REFERENCE	Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T., Jackson,C., Shin,I.T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J., Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F., Brasch,M.A., Vandenbussche,J., Lamesch,P.E., Hill,D.E., and Vidal,M.	
	Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact Jerome.reboul@dfci.harvard.edu or philippe.vaglio@dfci.harvard.edu	AUTHORS		
	POLY-A-No.	TITLE	Open reading-frame sequence tags (OSTS) support the existence of at least 17,300 genes in C. elegans	
	Location/Qualifiers	JOURNAL	Nat. Genet. 27 (3), 332-336 (2001)	
	1..477	COMMENT	21135099	
	/organism="Caenorhabditis elegans"	CONTACT	Contact: Reboul J, Vaglio P	
	/strain="N2"		Marc Vidal Laboratory	
	/strains="N2"		Dana Farber Cancer Institute	
	/db_xref="taxon:6239"		44 Binney Street, Boston, MA 02115, USA	
	/db_xref="Ad-wrmCDNA"		Tel: 617 632 5180	
	/clone_lib="Ad-wrmCDNA"		Fax: 617 632 2425	
	/sex="Hermaphrodite and male"		Email: Jerome.Reboul@dfci.harvard.edu	
	/tissue_type="whole animal"		Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact Jerome.reboul@dfci.harvard.edu or philippe.vaglio@dfci.harvard.edu	
	/dev_stage="mixed stage"			
	/note="The AD-wrmCDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauer and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86."			
FEATURES	source	BASE COUNT	131 a	109 g 150 t
		ORIGIN		
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		Best Local Similarity	99.2%	Pred. No. 7.7e-72;
		Matches	473;	Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	41 AACAGGAGGGAGGTGAGATGCCAACACATAACGTTACGGTACATCCTGATAA	41	AACAGGAGGGAGGTGAGATGCCAACACATAACGTTACGGTACATCCTGATAA	100
Db	1 AACAGGAGGGAGGTGAGATGCCAACACATAACGTTACGGTACATCCTGATAA	1	AACAGGAGGGAGGTGAGATGCCAACACATAACGTTACGGTACATCCTGATAA	60
Qy	101 CAATCGGAATAGCCAAAAGAACGAAAATGTTGGAAGAACGGGACTGAATAACGGAG	101	CAATCGGAATAGCCAAAAGAACGAAAATGTTGGAAGAACGGGACTGAATAACGGAG	160
Db	61 CAATCGGAATAGCCAAAAGAACGAAAATGTTGGAAGAACGGGACTGAATAACGGAG	61	CAATCGGAATAGCCAAAAGAACGAAAATGTTGGAAGAACGGGACTGAATAACGGAG	120
Qy	161 CATCTCACGTTATTCTCATTTGTCGGGTCACTATGATGGCTGTGTTGTTTA	161	CATCTCACGTTATTCTCATTTGTCGGGTCACTATGATGGCTGTGTTGTTTA	220
Db	121 CATCTCACGTTATTCTCATTTGTCGGGTCACTATGATGGCTGTGTTGTTTA	121	CATCTCACGTTATTCTCATTTGTCGGGTCACTATGATGGCTGTGTTGTTTA	180
Qy	221 CGATGAAACGATTAGTTTATAGTCAAACAAATGAAACCGATTACTACACATCCTT	221	CGATGAAACGATTAGTTTATAGTCAAACAAATGAAACCGATTACTACACATCCTT	280
Db	181 CGATGAAACGATTAGTTTATAGTCAAACAAATGAAACCGATTACTACACATCCTT	181	CGATGAAACGATTAGTTTATAGTCAAACAAATGAAACCGATTACTACACATCCTT	240
Qy	281 TTGTCGGGAACAGACAGATCGTGTGAGAGGGATTGATGTCATGGAAATGCCTCG	281	TTGTCGGGAACAGACAGATCGTGTGAGAGGGATTGATGTCATGGAAATGCCTCG	340
Db				
		Query Match	24.9%	Score 374; DB 13; Length 386;
		Best Local Similarity	99.7%	Pred. No. 4.2e-55;
		Matches	385;	Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy	937 AAATGTAACGAAATTCTCTAAAGTGAATGAAATGCAATGCTTCAACGACA	937	AAATGTAACGAAATTCTCTAAAGTGAATGAAATGCAATGCTTCAACGACA	996
Db				
		Query Match	24.9%	Score 374; DB 13; Length 386;
		Best Local Similarity	99.7%	Pred. No. 4.2e-55;
		Matches	385;	Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy	386 AAATGTAACGAAATTCTCTAAAGTGAATGAAATGCAATGCTTCAACGACA	386	AAATGTAACGAAATTCTCTAAAGTGAATGAAATGCAATGCTTCAACGACA	327
Db				

Qy	997	CAAACCTCTGGACTAAAGGGTGGAAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGAC	1056	Qy	397	AGTTTTATAAGCCTATTATGGAATGGCTTATTCAGAGTTCTCTCTTTCCCTA 4 56	
Db	326	CAAATCTCTGGATTAAGGGTGGACGGGCTAGCTGCTGAGACCAACTGTACAAGAC	267	Db	121	AGTTTTATAAGCTTATICATGGATGGCTTATTCAGAGTTCTCTCTTTCCCTA 180	
Qy	1057	GCCAATTTACAGGCCAACAGGAAAGAGGAGGGTGAACCTGGCTGGGAGACTC	1116	Qy	457	TTCACACATCATATGTGTCAGAAAGGTTCTGATGTTGCTCCACGGACTA 51 6	
Db	266	GCCAATTTACAGGCCAACAGGAAAGAGGAGGGTGAACCTGGCTGGGAGACTC	207	Db	181	TTCACACATCATATGTGTCAGAAAGGTTCTGATGTTGCTCCACGGACTA 240	
Qy	1117	ATTTCTACTCTGTCTCCCTGGCAAGGGTCACTGTAATTGACTGAAACAGACTAC	1176	Qy	517	TGGTTTGTGTTGACTGGTAACTATGGAGTTCTGGATGTTGATACATTGGAAA 576	
Db	206	ATTTCTACTCTGTCTCCCTGGCAAGGGTCACTGTAATTGACTGAAACAGACTAC	147	Db	241	TGGTTTGTGTTGACTGGTAACTATGGAGTTCTGGATGTTGATACATTGGAAA 300	
Qy	1177	GCTTGTTATGTGGCCATTCTTATGGTCTCTGCTTCAGGACTCATTTTACTTTGT	1236	Qy	577	GGCCATTCGTCCTGCAAGGTTTACCTTATACAATGTCGACTATGGCTCTGGTC	636
Db	146	GCTTGTTATGTGGCCATTCTTATGGTCTCTGCTTCAGGACTCATTTTACTTTGT	87	Db	301	GTCCTTCGTCCTGCAACAGTTTACCTTATACAATGTCGACTATGGCTCTGGTC	360
Qy	1237	AAACGAGCACTCCGGCTCTG -CAATTCATTTCTCGGACTCATTTTACTTTGT	1295	Qy	637	TATTAAGTACTCT 650	
Db	86	AAACGAGCACTCCGGCTCTGCTCAATTTCATTTCTCGGACTCATTTTACTTTGT	27	Db	361	TATTAAGTACTCT 374	
Qy	1296	ACCCCTGGATCATCCCCATTTGT	1321				
Db	26	ACCGCGTGGATCATCCCCATTTGT	1				
				RESULT 4			
				C47805	375 bp	mRNA	
				LOCUS	C47805	linear EST 18-OCT-11999	
				DEFINITION	C47805	mRNA,Strain N2 hermaphrodite embryo	
				ACCESSION	C47805	Caenorhabditis elegans cDNA clone y452b9 5', mRNA sequence.	
				VERSION	C47805		
				KEYWORDS	C47805..1	GI:2384058	
				SOURCE		EST.	
				ORGANISM		Caenorhabditis elegans.	
						Caenorhabditis elegans	
						Eukaryota; Metazoa; Nematoidea; Rhabditida; Rhabditoidae	
						Rhabditidae; Pelerodinae; Caenorhabditis.	
				REFERENCE		1 (bases 1 to 375).	
				AUTHORS		Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano	
						M., Miyata,A. and Nishigaki,A.	
				TITLE		Expression map of the C.elegans genome	
				JOURNAL		unpublished (1996)	
				COMMENT		Contact: Yuji Kohara	
						Genome Biology Lab.	
				FEATURES		National Institute of Genetics	
				source		Yata 1111, Mishima, Shizuoka 411, Japan	
						Tel: 81-559-81-6854	
						Fax: 81-559-81-6855	
						Email: yohara@lab.nig.ac.jp.	
						1. .375	
						/organism="Caenorhabditis elegans"	
						/clone_y452b9"	
						/clone_lib="Yuji Kohara unpublished cDNA:Strain N2	
						CDNA:Strain N2"	
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						Matches 373; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
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						Matches 373; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	
Qy	278	CTTGTGTCGGAAACAGAGATCTGTTGAGGGTGTCACTTGG -AAATGG	336	Qy	921	AAAGCCTAAAGCACAAACTCTGGAAAGGGCTAGCTGCTGAGAG	980
Db	1	CTTGTGTCGGAAACAGAGATCTGTTGAGGGTGTCACTTGG -AAATGG	60	Db	1	AAAGCCTAAAGCACAAACTCTGGAAAGGGCTAGCTGCTGAGAG	60
Qy	337	CTCGTCACTGTTGCGCTGGCTGTTCTGATGACAGCTTCGCTGATTGTTCTATAAAC	396	Qy	981	TACAGCTTCAAGCACAAACTCTGGAAAGGGCTAGCTGCTGAGAG	1040
Db	61	CTCGTCACTGTTGCGCTGGCTGTTCTGATGACAGCTTCGCTGATTGTTCTATAAAC	120	Db	61	TACAGCTTCAAGCACAAACTCTGGAAAGGGCTAGCTGCTGAGAG	120
						1041 ACACAATGTCACAGGCCAAATTCACAGCACCSAGAGAACAGAGGTGTTGAAACT	1100

Db	121 ACCAACTGACAAGCGCCAAATTTCACAGGCCAACATTTCAAGGCCAACAGAGAGGGTGTGAAACT	180	Qy	535 GGTAACTATGGAGTTCTCGGAATGATGTTATACATTGGAAAGGTCATTGGCTCTGGAA 594
Qy	1101 TGGCTGGGGACTCTCATTTCTACTCTGTTCTCCTGCCAAGGCTTATCGTACTTGA 1160		Db	181 GGTAACTATGGAGTTCTCGGAATGATGTTATACATTGGAAAGGTCATTGGCTCTGGAA 240
Db	181 TGGCTGGGGACTCTCATTTCTACTCTGTTCTCCTGCCAAGGCTTATCGTACTTGA 240		Qy	595 CAGTCTACCTTATACAGTGTGCACTTAATGGCTCTGGCTTATCAGTACTACCA 654
Qy	1161 CTGGACACGACTATCGCTGTGTTATGGCCATTCTTATCGGTCTGTTCACTCTGT 1220		Db	241 CAGTCTACCTTATACAGTGTGCACTTAATGGCTCTGGCTTATCAGTACTACCA 300
Db	241 CTGGACACGACTATCGCTGTGTTATGGCCATTCTTATCGGTCTGTTCACTCTGT 300		Qy	655 GAATGGACTGTGTGTTTGCTGTGTTGGATCTCGGTTGGATCTGTGCTGC 714
Qy	1221 CCTGCTGGCGTCTCAAAAGGACTCTGGGCTCTG-CAAATTCCATTTCTCCGGGACT	1279	Db	301 GAATGGACTGTGTGTTGGATCTCGGTTGGATCTGTGCTGC 360
Db	301 CCTGCTGGCGTCTCAAAAGGACTCTGGGCTCTGCAATTCCATTTCTCCGGGACT	360		
Qy	1280 CATTTTACTTT 1294			
Db	361 CATTTTACTTT 375			
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			AV186436	
			LOCUS	AV186436 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
			DEFINITION	embryo Caenorhabditis elegans cDNA clone yk499e3 5', mRNA sequence.
			ACCESSION	AV186436
			VERSION	AV186436.1 GI:5568419
			KEYWORDS	EST.
			ORGANISM	Caenorhabditis elegans.
			REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae ; Rhabditidae; Pelederinae; Caenorhabditis .
			AUTHORS	Kohari,Y., Shin-i,T., Thierry-Mieg,J., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitanii,Y., Iida,K., Nomoto,H.
			TITLE	Expressed genes in C.elegans
			JOURNAL	Unpublished (1999)
			COMMENT	Contact: Yuji Kohara . National Institute of Genetics Yata 1111, Mishima, Shizuoka 411, Japan Genome Biology Lab. Tel: 81-559-81-6854 Fax: 81-559-81-6855 Email: ykohara@ab.nig.ac.jp.
			FEATURES	1..360 /organism="Caenorhabditis elegans" /strain="N2" /clone_id="YK499E3" /db_xref="taxon:6239"
			source	
			Query Match	23.4%; Score 350.6; DB 9; Length 360;
			Best Local Similarity	98.3%; Pred. No. 4.9e-51;
			Matches	Mismatches 0; Indels 0; Gaps 0;
			ORIGIN	
			BASE COUNT	103 a 62 c 85 g 108 t 2 others
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			Query Match	52 GGAGCTGGAGATGGGGACACATACAGCTTACGGTAAATCTGATPACAAATCGGAAT 111
			Best Local Similarity	2 GGANGTGAGATGGGAACACATACCGTTACGGTAAATCTGATPACAAATCGGAAT 61
			Matches	353; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
			ORIGIN	
			BASE COUNT	
			ORIGIN	
			Query Match	24.0%; Score 360; DB 9; Length 360;
			Best Local Similarity	100.0%; Pred. No. 1.2e-52;
			Matches	Mismatches 0; Indels 0; Gaps 0;
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			Best Local Similarity	100.0%; Pred. No. 1.2e-52;
			Matches	Mismatches 0; Indels 0; Gaps 0;
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			BASE COUNT	
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			Best Local Similarity	100.0%; Pred. No. 1.2e-52;
			Matches	Mismatches 0; Indels 0; Gaps 0;
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			BASE COUNT	
			ORIGIN	
			Query Match	61 CATGGATGGCTTATTGTCAGCACTTTCCTCTCTTCTATAAATACAACTCTATG 120
			Best Local Similarity	100.0%; Pred. No. 1.2e-52;
			Matches	Mismatches 0; Indels 0; Gaps 0;
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			BASE COUNT	
			ORIGIN	
			Query Match	475 CAAGAAGTCTGAAAAGTTCTGATGTCCTCCAGGGACTATTGGTTGGACTG 534
			Best Local Similarity	100.0%; Pred. No. 1.2e-52;
			Matches	Mismatches 0; Indels 0; Gaps 0;
			ORIGIN	
			BASE COUNT	
			ORIGIN	
			Query Match	121 CAAGAAGTCTGAAAAGTTCTGATGTCCTCCAGGGACTATTGGTTGGACTG 180
			Best Local Similarity	100.0%; Pred. No. 1.2e-52;
			Matches	Mismatches 0; Indels 0; Gaps 0;
			ORIGIN	

Qy	292	ACAGACAGTATCGTTGAGAAGGGATTGATGTCACTTGTGAAATGCTCTCGTCATGTTGTC	351	Db	301	TCATGTTGCGTGGTCTGATGACAGTTCGCTGATTGTTCTATAAAATACAAGT	360
Db	242	ACAGACAGTATCGTTGAGAAGGGATTGATGTCACTTGTGAAATGCTCTCGTCATGTTGTC	301				
Qy	352	GTGGTCTGTTCTGATGACAGTTCGTTGATGTTCTATAAAATACAAGTGTATAAGCT	410	RESULT 8		374 bp mRNA linear EST 22-JUL-1999	
Db	302	GTGGTCTGTTCTGATGACAGTTCGTTGATGTTCTATAAAATACAAGTGTATAAGCT	360	AV192017 LOCUS	AV192017	Yoji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone Yk600e12 5', rRNA sequence.	
RESULT 7				DEFINITION	AV192017.1	EST	
LOCUS	AV198059	360 bp mRNA linear EST 26-JUL-1999		ACCESSION	GI:5574169		
DEFINITION	AV198059	Yoji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone Yk674e3 5', mRNA sequence.		VERSION	AV192017.1	EST	
ORGANISM	AV198059			KEYWORDS			
ORGANISM	AV198059.1			ORGANISM			
VERSION	EST.			REFERENCE	1	(bases 1 to 374)	
KEYWORDS	Caenorhabditis elegans.			AUTHORS	Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.		
SOURCE	Caenorhabditis elegans			TITLE	Expressed genes in C.elegans		
ORGANISM	Eukaryota; Metazoa; Nematoidea; Chromadorea; Rhabditida; Rhabditoidae; Rhabditidae; Peioderinae; Caenorhabditis.			JOURNAL	Unpublished (1999)		
REFERENCE	1 (bases 1 to 360)			COMMENT	Contact: Yoji Kohara		
AUTHORS	Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.			FEATURES	Genome Biology Lab.		
TITLE	Expressed genes in C.elegans			Source	National Institute of Genetics		
JOURNAL	Unpublished (1999)			Source	Yata 1111, Mishima, Shizuoka 411, Japan		
COMMENT	Contact: Yoji Kohara			Source	Tel: 81-559-81-6854		
ORGANISM	Genome Biology Lab.			Source	Fax: 81-559-81-6855		
FEATURES	National Institute of Genetics			Source	Email: ykohara@lab.nig.ac.jp.		
FEATURES	Yata 1111, Mishima, Shizuoka 411, Japan			Source	Location/Qualifiers		
FEATURES	Tel: 81-559-81-6854			Source	1. .360		
FEATURES	Fax: 81-559-81-6855			Source	/organism="Ceenorhabditis elegans"		
FEATURES	Email: ykohara@lab.nig.ac.jp.			Source	/db_xref="taxon:6239"		
FEATURES	Location/Qualifiers			Source	/clone_id="Yk674e3"		
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FEATURES	/dev_stage="embryo"			Query Match	22.8%		
FEATURES	/dev_stage="embryo"			Query Match	22.6%		
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FEATURES	/dev_stage="embryo"			Best Local Similarity	98.4%	Pred. No. 1.1e-49;	
FEATURES	/dev_stage="embryo"			Mismatches	0;	Mismatches 0;	
FEATURES	/dev_stage="embryo"			Mismatches	0;	Mismatches 0;	
FEATURES	/dev_stage="embryo"			Indels	2;	Indels 2;	
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FEATURES	/dev_stage="embryo"			Gaps	2;	Gaps 2;	
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Db	1	ACCAGGAGGGGGGGGGAGGTGGCATGCGGAACANATACCCGTTACNGTACAAATCGATA	60	Db	2	AGGAGGGGGGGGGTCAAGATGCGGTTACGGTACAAATCGATAACA	61
Qy	101	CAAATCGGAATAGCCAAGAACAGCAAAATTTGGGAAAGCGGGAGCTGAATACGGAG	160	Qy	103	AATCGGG-AATAGGCCAAGAGCACAAATGTTGAGAAGGGAGCTGAATACGGAGC	161
Db	61	CAAATCGGAATAGCCAAGAACAGCAAAATTTGGGAAAGCGGGAGCTGAATACGGAG	120	Db	62	AATCGGAATAGGCCAAGAGCACAAATGTTGAGAAGGGAGCTGAATACGGAGC	121
Qy	161	CATCTACGTTTATCATCPATTGTCGCGGTGTCACATCCATGCCTGGTTGTTTA	220	Qy	162	ATCTACGTTTATCATCTATTGTCGGGTTCTATGATGGCTCTGGTTTTAC	221
Db	121	CATCTACGTTTATCATCPATTGTCGCGGTGTCACATCCATGCCTGGTTGTTTA	180	Db	122	ATCTACGTTTATCATCTATTGTCGGGTTCTATGATGGCTCTGGTTTTAC	181
Qy	221	CGATGACAGCATTAGTTATAGCTAAAACAATGGAAGGGATTGATGTCACTTCCTT	280	Qy	222	GATGAAACAGCATAGTTTATAGCTAAAACAATGGAAGGGATTGATGTCACTTCCTT	281
Db	181	CGATGACAGCATTAGTTTATAGCTAAAACAATGGAAGGGATTGATGTCACTTCCTT	240	Db	182	GATGAAACAGCATAGTTTATAGCTAAAACAATGGAAGGGATTGATGTCACTTCCTT	241
Qy	281	TTGTCGGGAAACACAGCAAGATGTCGTTGATGTCAGTTGTCGTTGTTCTGATG	340	Qy	282	TGTCGGGAAACAGCAGTATGTTGAGAAGGGATTGATGTCACTTCCTG	341
Db	241	TTGTCGGGAAACACAGCAAGATGTCGTTGATGTCAGTTGTCGTTGTTCTGATG	300	Db	242	TGTCGGGAAACAGCAGTATGTTGAGAAGGGATTGATGTCACTTCCTG	301
Qy	341	TCATGTTGTCGGGCGTCTGATGACAGTTCGTTCTGATGTCAGTTGTTCTATAAA	400	Qy	342	CATGTTGTCGGGCGTCTGATGACAGTTCGTTCTGATGTCAGTTGTTCT	401
Db				Db	302	CATGTTGTCGGGCGTCTGATGACAGTTCGTTCTGATGTCAGTTGTTCT	361
Qy				Db			
Qy				Qy			

Db	110	TGTACCCGCTGGATATCACCCCCATTGTACACAGTCTCAAAAGTTTATTATA	1	DEFINITION	AV175978 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone Yk499e3 3', mRNA sequence.
QY	1353	TAATTCCTCTCTTTCGCCATTTCGCATCATCAACTTTCGATTATAT 1402		ACCESSION	AV175978.1 GI:5555879
Db	50	TAATTCCTCTCTTTCGCCATTTCGCATCATCAACTTTCGATTATAT 1		VERSION	
ACCESSION				KEYWORDS	
VERSION				ORGANISM	Caenorhabditis elegans
REFERENCE				COMMENT	Caenorhabditis elegans Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoidea ; Rhabditidae; Pejoderaiae; Caenorhabditis.
AUTHORS				REFERENCE	1 (bases 1 to 300)
ORGANISM	C34382	300 bp mRNA linear EST 18-OCT-1999		AUTHORS	Kohara,Y., Shin-I,T., Thierry-Mieg,J., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Sugiyama,Y. and Nomoto,H.
DEFINITION	C34382	yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo		JOURNAL	Expressed genes in C.elegans
Caenorhabditis elegans	C34382	Caenorhabditis elegans cDNA clone Yk400e3 3', mRNA sequence.		COMMENT	Unpublished (1999) Contact: Yuji Kohara Genome Biology Lab.
Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoidea	C34382	Rhabditida; Pejoderaiae; Caenorhabditis.		NATIONAL INSTITUTE OF GENETICS	National Institute of Genetics Yata 1111, Mishima, Shizuoka 411, Japan
Rhabditidae; Pejoderaiae; Caenorhabditis.	C34382	(bases 1 to 300)		CONTACT	Yata 1111, Mishima, Shizuoka 411, Japan
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.	C34382.1	EST.		TELEPHONE	81-559-81-6834
Expression map of the C.elegans genome				FAX	81-559-81-6855
Unpublished (1996)				EMAIL	ykohara@lab.nig.ac.jp.
COMMENT				LOCATION/QUALIFIERS	Location/Qualifiers 1. .300 /organism="Caenorhabditis elegans" /strain="N2" /db_xref="taxon:6239" /clone_id="Yk499e3" /clone_lib="Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo" /sex="hermaphrodite" /dev_stage="embryo"
KEYWORDS				BASE COUNT	118 a 44 c 80 g 56 t 2 others
ORGANISM				ORIGIN	
DEFINITION	C34382	300 bp mRNA linear EST 18-OCT-1999		QUERY MATCH	Score 268 8; DB 9; Length 300;
Caenorhabditis elegans	C34382	yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo		BEST LOCAL SIMILARITY	97.7%; Pred. No. 7.3e-37;
Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoidea	C34382	Caenorhabditis elegans cDNA clone Yk400e3 3', mRNA sequence.		MISMATCHES	0; Mismatches 4; Indels 3; Gaps 2;
Rhabditidae; Pejoderaiae; Caenorhabditis.	C34382	(bases 1 to 300)		QY	1114 TTCAATTCTACTCTGTTCTCGCAAGGCCATCGTACTTGACTGGAACAGCAGCT 1173
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.	C34382.1	EST.		DB	299 TTCAATTCTACTCTGTTCTCGCAAGGCCATCGTACTTGACTGGAACAGCAGCT 240
Expression map of the C.elegans genome				QY	1174 ATCGCTTGTATGGCCACPTTATCGGCTCTGCTTCACTTGCTGCTCGCCGTC 1233
Unpublished (1996)				DB	239 ATCGCTTGTATGGCCACPTTATCGGCTCTGCTTCACTTGCTGCTCGCCGTC 181
COMMENT				QY	1234 TTCAAACGAGCACTCCGGCTCTGC - AATTCCATTCTCGGACTCTTACTT 1291
Contact: Yuji Kohara				DB	180 TTCAAACGAGCACTCCGGCTCTGCCTAATTCGGAATTCGCAATTCGACTCTTACTT 121
Genome Biology Lab.				QY	1292 TTGTACCGCGCTGATCATCACCCATTGGTACAAGTCCTCAAAAGTGTATTATA 1351
National Institute of Genetics				DB	120 TTGTACCGCGCTGATCATCACCCATTGGTACAAGTCCTCAAAAGTGTATTATA 61
Yata 1111, Mishima, Shizuoka 411, Japan				QY	1352 TTAATCTCTGTTTGCCATTTCGATCATCAACTTTGATTATATCTTGGCGCA 1411
tel: 81-559-81-6834				DB	60 TTAATCTCTGTTTGCCATTTCGATCATCAACTTTGATTATATCTTGGCGCA 1
Fax: 81-559-81-6855				RESULT	18
Email: ykohara@lab.nig.ac.jp.				LOCUS	AV17958/c
FEATURES				DEFINITION	AV17958 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone Yk600e12 3', mRNA sequence.
SOURCE				ACCESSION	AV17958
				VERSION	AV17958.1 GI:5559859
				KEYWORDS	Caenorhabditis elegans
				ORGANISM	Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoidea
RESULT	17	AV175978/c	AV175978	LOCUS	

Db	636	AATGCTGGTAGAAACTGCCAGGAGAAAATGACCCCATATTCCCTGCCCTGATATAC	TCT 635	Qy	328	GAATGCTCTGCATGTTGGCTGGTCTGATGACAGTCTGCTGATGTTTC	387
Qy	795	GTCIG 799		Db	185	CTGACACCTCACATGTCAGGTCACTGTTTATGCTGCTGATGTC	244
Db	696	ATCTG 700		Qy	388	TATAATAAACAGTTTATAAGCTTATTATGGATGGCTTATTGTCAGCAGTTCTCT	447
				Db	245	TACAGTACCGTGTGCTACAGTCACTCCATGGTGTGATCATGTCITACGTGCTG	304
RESULT	20			Qy			
LOCUS	AI675803	AI675803	661 bp mRNA linear EST 17 DEC-1999	Qy	448	CTTTCCTTAATCACTACAATCTGCAAGAAGTTCGAACTGTC	507
DEFINITION	wb9ta12.x1	NCI_CGAP_Pr28	Homo sapiens cDNA clone IMAGE:2313598 3	Qy	305	CTGTTCTCTACCTATACCTGTCAGCTACAGCTACATGTCATGCTCATG	364
	similar to SW:PSN2_HUMAN	P49810 PRESENTLIN 2 ; mRNA sequence.		Db			
ACCESSION	AI675803	AI675803.1	GI:4876283	Qy	508	AGGCCACTATTGGTTGGACTGGAACTGGTAATATGGAGTTCTGGAATGTTGATA	567
VERSION				Db	365	GACTACCCACCCCTTGCTGACAGTCGGCATGGCAGTGGCATGGTC	424
KEYWORDS				Qy	568	CATTCGAAAGGTCATTGCTGCAACAGTTACCTTATTACATGTCGACTAATG	627
SOURCE	Human.			Db	425	CACTGGAAAGGCCCTCTGGTGTGAGCAGGCCATCTCATGTCATGCTCATG	484
ORGANISM	Homo sapiens			Qy	628	GCTCGTGTCTTATAAGPACCTTACAGATGACTGTGCTGTTGTTATTC	687
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Db	485	GCCCCATGGTCTCATGACCTTCCAGACTGGCTGGCTCATGGGCCCATC	544
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				Qy	688	TGCGTTGGATCTGGTCTGCTCACACAAAAAGGACCATGAGATATTGGGAA	747
1 (bases 1 to 661)				Db	545	TCTGTTGATGATCCTGTCGCTGTGTCAGTCAGAATGCTGCTAGAA	604
NCI-CGAP http://www.ncbi.nlm.nih.gov/nicgap.				Qy	748	ACTGCACAGSAGAGAACAGGCCAATTTCGGGGCTGATTATTCGCTG	799
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			Db	605	ACTGCCAGGAGAGAANTGAGCCCATATTCCTGCTGTATACTCATCTG	656
TITLE	Tumor Gene Index						
Unpublished (1997)				RESULT	21		
COMMENT	Unpublished (1997)			A1925372			
Contact: Robert Strausberg, Ph.D.				LOCUS			
Email: cgaps-re@mail.nih.gov				DEFINITION	wn53d06.x1	NCI_CGAP_Lu19	703 bp mRNA . linear EST 02-SEP-1999
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.				REFERENCE			
Emmert-Buck, M.D., Ph.D.				AUTHORS			
CDNA Library Preparation: M. Bento Soares, Ph.D.				TITLE			
CDNA Library Arrayed by: Greg Lennon, Ph.D.				ACCESSION	A1925372		
DNA Sequencing by: Washington University Genome Sequencing Center				VERSION			
Clone distribution: NCI-CGAP Clone distribution information can be				KWONDS			
found through the I.M.A.G.E. consortium/LUUL at:				SOURCE			
www-bio.lnl.gov/bbry/image/image.html				ORGANISM			
Insert Length: 1317 Std Error: 0.00							
Seq primer: -40UP from Gibco							
High quality sequence stop: 461.							
Location/Qualifiers							
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/dev_stage="adult"							
/lab_host="DRI10B"							
/note="Organ: prostate; Vector: pTT3D-Pac (Pharmacia)							
with a modified polylinker; Plasmid DNA from the							
normalized library NCI_CGAP_Pr22 was prepared, and ss							
circles were made in vitro. Following HAP purification,							
this DNA was used as tracer in a subtractive hybridization							
reaction. The driver was PCR-amplified cDNA from a pool							
of 5,000 clones made from the same library (cloneIDs							
985608-986759, 1101192-1101959, and 1217938-1220615).							
Subtraction by Bento Soares and M. Fatima Bonaldo.							
BASE COUNT	132 a	190 c	166 g	2 others			
ORIGIN							
Query Match	14 6%	Score 219;	DB 9;	Length 661;			
Best Local Similarity	59.5 %	Pred. No. 1.9e 28;					
Matches	388;	Conservative 0;	Mismatches 261;	Indels 3;	Gaps 1;		
Db	8	CTCAAAATACGGACGAACTCGTATTCACTGTTGCTGACTATGGCT 207					
Qy	148	CTGAAATACGGACGAACTCGTATTCACTGTTGCTGACTATGGCT 67					
Db	208	CTGGTTGTTTACGATGACAGTAAACAGATGAAAGGCTATGTTA 267					
Qy	68	GTGGTGTGACGACATTCAGTCACTGTTGCTGACTATGGCT 124					
Db	268	CTATCACATCCCTTGTCCGGAAACAGACAGTCACTGAGAAGGGATGATGTCAC 327					
Qy	125	ATCTACAGCCATTCACTGAGACACACCCCTGGCCAGCCTCAACTCCGTRG 184					

Qy	719 CAAAGGACCATGGAGATATTGGTGAAGAACGAGGAAACTGCACAGGAGAGAAACGAGCCAATTTC 777	Qy	479 AAGTTCTGAAAGTTTCGATGTGTCCTCCAGGCCACTATTGGTTGGACTGGATA 538		
Db	931 CGAAACKCCACTTCGTATGGTTCAGGAGAATGAAACGCTTTTC 987	Db	710 AAGTGTITTAACCTATAACGTGCTGGACTACATTACTGACTCTGAACTCTGG 769		
RESULT 25		Qy	539 ACTATGGAGTCTCGGAATGATGTGATACTGGAAAGGTCATGTGCTGTCACAGT 598		
LOCUS	AL553084 977 bp mRNA linear EST 16-FEB-2001	Db	770 ATTTCGTGTTGGCAATGATTTCATTCACTGGAAAGGTCACTTGACTCCAGG 829		
DEFINITION prime, mRNA sequence.		Qy	599 TCTACCTTATACAATGTCGCACTATGGCTCTGTCATGTTACAGTACCAAGAT 658		
ACCESSION AL553084	LT1_NFL006_PL2 Homo sapiens cDNA clone CS001074vD06 5	Db	830 CATATCCATATGATTAGTCCTGCTGTTATCAGTACCTCCCTGAAT 889		
VERSION AL553084.1	GI:12892590 EST.	Qy	659 GRACTGTGTTGGCTGTTGTTGATCTGGTTGGATGTGTTGGATGTTGCTCACAC 718		
SOURCE ORGANISM Homo sapiens		Db	890 GGACTCGTGGCTCATCTGGCTGTTGATTGATGTTGAGATTTGGTGA 949		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 97)	Qy	719 CAAAAGGACCATGGAGATTTGGTGA 746		
REFERENCE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		Db	950 CGAAAGGCCACTCGTGTGTTGAA 977		
AUTHORS	Full-length cDNA libraries and normalization	RESULT 26			
TITLE Unpublished (2001)		AW604230	AW604230		
JOURNAL Contact: Genoscope	Genoscope - Centre National de Sequençage	LOCUS	IL3-CT0129-210100-059-C04		
COMMENT BP 191 91.006 EVRY cedex - France	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	DEFINITION	CT0219_Homo_sapiens_CDNA, mRNA sequence.		
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source	1..977	KEYWORDS	EST.		
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	/db_xref="taxon:9606"		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	/clone="CS001074vD06"	REFERENCE	1 (bases 1 to 705)		
	/clone_lib="LT1_NFL006_PL2"	AUTHORS	HCGP		
	/tissue_type="placenta"	TITLE	http://www.ludwig.org.br/ORESTES.		
	/note="Vector: PCMVSPORT 6; Site:1: NotI; 1st strand CDNA was primed with a NotI-OligodT primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"	JOURNAL	The FAPEESP/LICR Human Cancer Genome Project Unpublished (1999)		
BASE COUNT	238 a 222 c 249 g 267 t 1 others	COMMENT	Contact: Simpson A.J.G.		
ORIGIN			Laboratory of Cancer Genetics		
			Rua Prof. Antônio Prudente 109, 4 andar, 01509-010, São Paulo-SP, Brazil		
			Tel: +55-11-2704922		
			Fax: +55-11-2707001		
			Email: asimpson@ludwig.org.br		
			This sequence was derived from the FAPEESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?pt=IL3&t=IL3-C0219-210100-059-C04&t3=2000-01-21&t4=1)		
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			High quality sequence stop: 599.		
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			/clone_lib="CM0219"		
			/dev_stage="Adult"		
			/note="Organ: colon; Vector: puc1b; Site:1..Site:2: Smal I: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 1,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
			BASE COUNT		
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			ORIGIN		
Query Match	13.7%	Score 205.2; DB 9; Length 977;	Query Match	13.6%	Score 204.2; DB 10; Length 705;
Best Local Similarity	58.9%	Pred. No. 3.8e-26;	Best Local Similarity	60.9%	Pred. No. 6.7e-26;
Matches 370;	Conservative	Indels 254; Gaps 1;	Matches 332;	Conservative 0;	Mismatches 213; Indels 0; Gaps 0;
Qy	119 AAGACCAAATGTTGGAGAACGGCTGAAATACGGACATCTCAGTTATC 178	Db	473 TTATGTCGCGGTGACTARGCATGCGTCGTTTACGAGAACGATTA 238		
Db	353 AAGATGAGGAAGATGAGGAGTCACATGAAATAATGGCCAAAGCATG 412	Qy	419 GATGGCTTATGTCAGCAGTTCATCTCTCTTCTTCCATTCACTACAACTCTATGTCAG 478		
Qy	179 TATTGTCGCGGTGACTARGCATGCGTCGTTTACGAGAACGATTA 238	Db	590 TTGTCTGACTATCCCTGGTCTGTTAATACGGCTTAAGGTCACTCATG 649		
Db	413 TCTTTCGTCCTGTCATGGTCTGTCATGTTGCTGTTGCTACCATTAAGTCAGCT 472	Qy	530 CTGTGCCAGAGGCCCTGCACCTCAATTCTGAATCAGGATCACTGTCATTG 589		
Qy	239 TTATACCAAAATGAGGCAATTACTATCACATGCCCTTTCGCGGGAAACAGACA 298	Db	359 TTCTGATGACAGTCGTCGTTCTATACATCACATGCCCTTTCGCGGGAAACAGACA 418		
Db	473 TTATACCGGAGGGTG--GGCACCTAACTATACCCATTCAAGAAAGATACCGAGA 529	Qy	591 ATGGAAAGGCATTACTATCACATCCCTGGTCTGTTAAGGTCACTCATG 649		
Qy	299 GTATCGTTGAGAAGGGATTGATGTCACCTGGAAATCTCTGTCATGTTGCTG 358	Qy	253 ATGGAAAGGCATTACTATCACATCCCTGGTCTGTTAAGGTCACTCATG 312		
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31	AGGATGGCACCTAACTATCACAGANGATACCGAGACTGTGGGCCAGAGGA	90		
313	GGATTGATGTCACCTGGAAATGCTCCTCGTCATGTTGCGTGGCTCTCATGACAGAT	372	FEATURES	seq primer: puc 18 forward High quality sequence stop: 635.
91	GCCCTGCACCTAACTCTGAATGCTGCCATCATGTCATGTCATGACTATC	150	source	Location/Qualifiers 1. 733
373	CNGCTGATGTTCTTCTATAAATACAAGTTTAACTGATGATGCTTATTGTC	432		/organism="Homo sapiens" /clone_id="CN0219" /dev_stage="Adult" /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 '716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
151	CTCCCTGGTCTGCTGATAATACAGTGCTATAAGTCTCATGCCGCTTATTATA	210		
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211	TCTATCTATGTTGCTGTCATTCTTCACTACTGGGAAGCTTTAACCC	270	ORIGIN	
493	TTCGATSTGTCTCCCAGGCCACTATGGTTGGACTTGGTAACATGGAGTTCTC	552	Query Match	13.6%; Score 204.2; DB 10; Length 733;
271	TATAACCTTGTGTTGACTACATTACTGTGTCACPTCTGATCTGGAAATTGGTGGT	330	Best Local Similarity	60.9%; Pred. No. 6.5e-26;
553	GGATGATGTTACATGGAAAGGCTCATGGGTTCTACGTTTACCTTATACA	612	Matches	Mismatches 213; Indels 0; Gaps 0;
331	GGATGATTTCCATTACTGAAAGGTCAATTGCTCAAGCCATATCTCATTATG	390	Qy	253 AATGGAGGCATTACTATCACATCCTTGTCCGGAAACAGACAGTACGTTGAGAAG 312
613	ATGTCGCACTAATGGCTCTGTTATCAAATGGACATGGTGTGGTT	672	Db	31 AAGGGATGGCAGCTATCTATACCCCATTCACAGAGATACCGGAGACTGGCCAGAGA 90
391	ATTAGTGCCTGCTGTTATCAAGTACCTCCGTGAATGGATCTGGCT 450		Qy	313 GGATTGATGTACTTGGAAATGCTCCTCGTCATGTTGCTGTTCTGATGAGATT 372
673	GTGCTGTTGTTATCCTGGTTGGATCTGGCTGTCACACCAAAAGGACATTG	732	Db	91 GCCCTGCACTAACTGAAATGCTGCAATCTGATGTCATGTCATGACTATC 150
451	ATCTTGCTGCTGATTGCAATTGATGTCATGTTGCTGTTGTCGCAAAGGTCCACTT	510	Qy	373 CTGCTGATTGTTCTATAAATACAGTTTATAACCTTATTCTGATGGCTTATGTC
733	AGATATTTGGTGGAAACTGACAGGAGAAACGAGCCAATTTCGGGGCTGATTТА	792	Db	432 151 CTCCCTGGTGTGTTGATAAAACAGGTGTGTTGCTCACTGCTCATTTA 210
511	CCTATGTTGTTGAAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC	570	Qy	433 AGCAGTTTCTCTCTTCTCTTCTTACTACAACTATGTCGAAAGTCTGAAAGT 492
793	TGTC 797		Db	211 TCTATCTATGCTGTCCTTCTTCTTCACTACTATGAGGTCTC 552
571	TCCTC 575		Qy	493 TTCACTGTTGCTGTCCTCCAGCCTACATTACTGTGTCACCTCTGTTGCTG 330
553	GGATGATGTTACATGGCTCTGGCTTATCAAGTACTACCTACAGAAGTCTGAAAGT 672		Db	271 TATARGTTGCTGTCCTACATTACTGTGTCACCTCTGTTGCTGAAATTGGTGTG 330
331	GGATGATTTCCATTACTGAAAGGTCAATTGCTCAAGCCATATCTCATTATG	390	Qy	553 GGAATGATGTTACATGGAAAGGCTCATTCAGTGGGAAAGTGTCTAAACC 270
613	ATGTCGCACTAATGGCTCTGTTATCAAATGGACATGGTGTGGTT	672	Db	391 ATTAGTGCCTCATGGCCCTGGTGTATCAAGTACTCTCCGTGAATGGACTGGCTG 450
673	GTGCTGTTGTTATCCTGGTTGGATCTGGCTGTCACACCAAAAGGACATTG	732	Qy	673 GTGCTGTTGTTATCCTGGCTGTCACACCAAAAGGACATTG 732
451	ATCTTGCTGCTGATTGCAATTGATGTCATGTTGCTGTTGTCGCAAAGGTCCACTT	510	Db	331 GGAATGATTTCCATTACTGAAAGTCCACTCTGTTGCTGAAATTGGTGTG 330
Qy	733 AGATATTTGGTGGAAACTGACAGGAGAAACGAGCCAATTTCGGGGCTGATTТА		Qy	673 ATGTCGCACTAATGGCTCTGGCTTATCAAGTACTACCTACAGAAGTCTGAAAGT 672
Db	511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC	570	Db	391 ATTAGTGCCTCATGGCCCTGGTGTATCAAGTACTCTCCGTGAATGGACTGGCTG 450
Qy	793 TCGTC 797		Qy	673 GTGCTGTTGTTATCCTGGCTGTCACACCAAAAGGACATTG 732
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RESULT 27			Qy	733 AGATATTTGGTGGAAACTGACAGGAGAAACGAGCCAATTTCGGGGCTGATTТА
DEFINITION			Db	511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
TL3-CT0219-160200-063-A06	733 bp	mRNA	Qy	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
AW850631	CT0219	Homo sapiens	Db	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
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ORGANISM			Qy	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Db	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			Qy	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
(bases 1 to 733)			Db	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baiu, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			Qy	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			Db	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
JOURNAL			Qy	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
MEDLINE			Db	570 511 CGTATGCTGGTGAACAGCTCAGGAGAAATGAACGGTTTCCAGGCTCTCAATTAC
COMMENT			RESULT 28	AW367465
Contact: Simpson A.J.G.			AW367465	AW367465
Ludwig Institute for Cancer Research			LOCUS	AW367465
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo - SP,			DEFINITION	MRO-HT0164-081199-007-c09
Brazil			ACCESSION	AW367465
Tel: +55-11-2704922			VERSION	AW367465.1
Fax: +55-11-2707001			KEYWORDS	EST.
Email: asimpson@ludwig.org.br			SOURCE	Homo sapiens
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL http://www.ludwig.org.br/scripts/gethtml?pi?1=&ts=1			ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
2000-063-A0653-2000-02-16&t=1				

Db	517	CGTATGCTGGTGAACAGCTCAGGGAGAAATGAAACGCTTTCAGCTCTCATTTAC	576
Qy	793	TGTCCTGGAGT	803
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RESULT	29		
AW604295			
LOCUS	AW604295	640 bp	mRNA linear
DEFINITION	IL3-CT0219-280100-062-A04	CP0219	Homo sapiens cDNA, mRNA sequence.
ACCESSION	AW604295		
VERSION	AW604295.1	GI: 7309036	
EST.			
SOURCE	human.		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 640)		
AUTHORS	HCGP	http://www.ludwig.org.br/ORESTES.	
TITLE	The FAPESP/LICR Human Cancer Genome Project		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br		
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?ID=IL3&t2=IL3-CT0219-280100-062-A04&t3=2000-01-28&t4=1)			
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SmaI; A mini-library was made by cloning products derived			
from ORESTES PCR (U.S. Letters Patent application No. 196			
,716 - Ludwig Institute for Cancer Research) profiles			
into the PUC 18 vector. Reverse transcription of tissue			
mRNA and cDNA amplification were performed under low			
stringency conditions."			
BASE COUNT	149 a 139 c 148 g 204 t		
ORIGIN			
Query	Match	13.5%	Score 203.2; DB 10; Length 640;
Best Local Similarity	60.7%	Pred. No. 1e-25;	
Matches	331;	Missmatches 214; Indels 0; Gaps 0;	
Qy	253	AATGGAAAGGCATTACTATCACCTTGTGGAAAACAGACAGTATCCGGTGTGAGAG	
Db	58	AAGGATGGCAGCTTAATCTAACCCATTCAAGAAAGATCCGGCAAGA	
Qy	313	GATTGATGTCATTGAAATGCTCTGCACTGTTGCGTGTGAGCTTGTGACAGTT	
Db	118	GCCTCTGGCACTCAATTCTGAATGTCGGCATCAGTCAATTGTCATTGTCATGCTATC	
Qy	373	CTCTCTGATTGTTCTATAATACAAGTTTATAAGCTTATTCATGGATGGCTTATGGTC	
Db	178	CTCTCTGGTGTCTGTTAAATPACAGGTGCTATCAGTCATCCATGGCTTATATA	
Qy	433	ACGAGTTTCTCTCTTCTCTTACTAACATTCTGCAAGAAGTCGTGAAAGT	
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180	a	149	c
		166	g
		218	t
		1	others

Oy	613	ATGTCGCACTAATGGCTCTGCTTATCAAGTACCTACCAAGATGGACTGTGCGTT	672		Matches 349; Conservative 0; Mismatches 223; Indels 3; Gaps 1;
Db	391	ATTAGTCCTCTATGCCCTGGTATAAGTACTCCCTGAATGACTGCTGCRC	450	Qy	223 ATGAAACAGATTACGTTTATAGTCAAAATGGAGGGATTACTATCACATCCTTAT 282
Oy	673	GTCGCTTGTGTTATCTCGGTTGGGATCTGGTGCCTCACACCAAAGGACCATG	732	Db	2 ATGAACTCAATCAGCTTATACCCGAAAGAT -GGAGCTTAATCTATACCCATTG 58
Db	451	ATCTTGCTGATTCAGATATGATTTAGGGCTTGTGTCGAAAGGTCACRPT	510	Qy	283 GTCCGGAAACAGACAGTATCGTGAAGGATGTCACCTGGAATGCTCTCGTC 342
Oy	733	AGATATTTGGTGAACACTGACAGGAGAGAACGCACTTTCGGGGCTGATTAT	792	Db	59 ACAGAAGATACCGAGACTGGCCAGAGGCCGCAATCTGAACTGTCACATTC 118
Db	511	CGTATGCTGGTAGATTCAGATATGATTTAGGGCTTGTGTCGAAAGGTCACRPT	570	Qy	343 ATGTTGCGTGGTGGTGTGATGACAGCTGCTGAGATGTTCTATAATAAGAGTT 402
Qy	793	TGTC 797		Db	119 ATGATCAGTGCATGTTGTCATGACTATCCTCCNGTGTGTTCTGATAATAACAGGTGC 178
Db	571	TCTCTC 575		Qy	403 TATAAGCTTATTATGAGATGGCTATTATATCATCTATGTCATGAGTTCTCTCTATTACTATGTCGCTGTTCTTTC 238
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RESULT 33				Db	179 TATAAGCTTATTATGAGATGGCTATTATATCATCTATGTCATGAGTTCTCTCTATTACTATGTCGCTGTTCTTTC 238
AWB850727	AWB850727	AN850727	573 bp	Qy	463 ACAATCTATGCAAGAAAGTCTGAAAGTTCGATGTGGCTCCAGCGACTATTGGTT 522
LOCUS	IL3-CT0219-160200-064-H05	CT0219	mRNA	Db	239 TTCAATTACTGGGGAAAGTGTAAACCTATAACGTTGCTGTTGACTATTTCTGT 298
DEFINITION	EST	AN850727	linear	Qy	523 TTGTTGGACTGGTAACATGGGATTCTGGATGATGTTACATGGAAAGGTCCA 582
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SOURCE	human.			Db	359 CTTGCACTCCAGGGCATATCTCATTATGATTAGTGCCTCATGGCCCTGGCTTTATC 418
ORGANISM	Homo sapiens			Qy	643 AAGTACCTTACGAATGGACTGTGGTTATCTCGGTGTTGGGATCTG 702
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Db	419 AAGPACCTCCCTGATGGACTGCCGTCATCTGGCTGTGATTCAGTATGATTTA 478
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				Qy	703 GTCGCGTGTCTCACACCAAAGGCCATTGAGATAATTGGTGGAAACTGCACAGGAGAGA 762
1 (bases 1 to 573)	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,			Db	479 GTGCGTGTGGTTGTGTCGAAAGGCCACTCGTGTGTTCTGAGTGTGTTCTG 538
KEYWORDS	Bordin, S., Costa, F.P., Zago, M.A., Bordim, S., Simpson, D.H.,			Qy	763 AACAGGCCAAATTTCGGCGCGMCATTATTGCG 797
SOURCE	Nagai, M.A., da Silva, W. Jr., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,			Db	539 AATGACACCCCTTTCCAGCTCTCATTTACTCC 573
REFERENCE	Goldman, G.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jonquieres, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.P., de Souza, S.J. and				
AUTHORS	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
TITLE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
JOURNAL	Contact: Simpson A.J.G.				
MEDLINE	Ludwig Institute for Cancer Research				
COMMENT	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil				
	Tel: +55-11-2704922		RESULT 34		
	Fax: +55-11-2707001		AWB04307		
	Email: asimpson@ludwig.org.br		LOCUS	AWB04307	601 bp mRNA linear EST 23-MAR-2000
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?pt1=612-pt2=IL3-CT0219-160200-064-H05&t3=2000-02-16t4=11)		DEFINITION	IL3-CT0219-280100-062-D09	Human sapiens CDNA, mRNA sequence.
FEATURES	Seq primer: puc 18 forward		ACCESSION	AWB04307	
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	/dev_stage="Adult"		TITLE	The FAPESP/LICR Human Cancer Genome Project	
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	Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196		COMMENT	Contact: Simpson A.J.G.	
	716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		REFERENCE	Laboratory of Cancer Genetics	
BASE COUNT	130 a		AUTHORS	Ludwig Institute for Cancer Research	
ORIGIN	127 c		TITLE	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil	
	127 g		JOURNAL	Tel: +55-11-2704922	
Query Match	Score 202.2; DB 10;		COMMENT	Fax: +55-11-2707001	
Best Local Similarity	Pred. No. 1..6e-25;		REFERENCE	Email: asimpson@ludwig.org.br	
	Length 573;		AUTHORS	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?pt1=613-ct0219-062-d09)	
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			JOURNAL	Seq primer: puc 18 forward	
			COMMENT	High quality sequence stop: 600.	
			REFERENCE	Location/Qualifiers	

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2. .601 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="CT0219" /dev_stage="Adult" /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 19716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplifications were performed under low stringency conditions."	138 a ASE COUNT ORIGIN	135 g 1 others		
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	253 AATGGAAGGGATTACTATCACATCCTTTGTCCGGAAACAGAAAGTAGATCTGGTGAAGAG 312 31 AAGGATGGCCGGCTTAATCTPATACATCCCATTCACAGAGATACCGAGACTGGGCCGAGA 90			
	313 GGATTGATGTCACTTGGAAATGCTTCGTCATGTTGTCGGTCTGATGAGACTT 372 91 GCCCCGACCAATTCTGAATGCTGCCATATGACAGTCATGTTGTCATGACTATC 150			
	373 CTGCTGATGTTCTCTATAATACCAAGTTTATAAGCTTATTCAGGATGGCTTATGTC 432 151 CTCGCCGGTGTCTGCTCTATAATACAGGTGCTTATAGGTCTGCCTGCTTATAATA 210			
	433 AGCAGTTCTCTCTTCTTCTTACTACATACATCTATGCAAGAAGTCTGAAAGT 492 211 TCATCTCTATGTTCTGCTGTTCTTTCATTCATTCTTACTTGGGAAAGCTTAAACC 270			
	493 TTTCGATGTTGCTCCAGCGCACTATGGTTTGTGACTGGTAACTATGGAGTTCTC 552 271 TATACTGTTGCTGTTGACTACATTGTTGCACTCTGATGGGATTGGTGTGTTG 330			
	553 GGAATGATGTTGATCATGGAAAGTCCATTGGCTGAAACAGTCTACCTTATTACA 612 331 GGAATGATTCTCATCTACTGGAAAGTCCATTCTACCTCCAGGCCATACCTCAATTATG 390			
	613 ATGTTGCACTAATGCTCTGCTTATCAAGTACCTACAGAAATGGACTCTGGTTT 672 391 ATTATGCCCCCTCATGGCCCTGGTTTATCAAGTACCTCCCTGATGGACTCTGGCTC 450			
	673 GTGCTGTTGTTATCTGGATCTGGATCTGGTGGCTCACACCAAAAGGCCATTG 732 451 ATCTTGCTGCTGATTCAGTATGTTGTCGAAACAGTCANAGAGAATGGAAAGTC 510			
	733 AGATTTGGGAAACTGACAGGAGAGAACGCCAAATTTCGGGGCTGATTAT 792 511 CGTATGCTGTTGAAACAGTCANAGAGAATGGAAAGCTCTCACTTAC 570			
	793 TCGTC 797 571 TCCTC 575			

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordim,S., Costa,F.F., Goldmann,G.H., Carvalho,A.F., Matsukuma,A., Bajia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongenelis,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.	TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	JOURNAL	proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2002663	MEDLINE	
Contact: Simpson A.J.G.	COMMENT	
Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP, Brazil		
tel: +55-11-27049222 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br		
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=IL3-Ct0219-160200-0402&t3=2000-02-16&t4=1)		
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159 c 181 g 223 t	BASE COUNT	193 a 159 c 181 g 223 t 1 others
ORIGIN		

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Qy	677	TGTTTGTTACCTCGGTTGGGATCTGGTTCCCTGATGGCTGGCTCATCC	736	Db	9	TACCATTAAGTCAGTCAGTTTAACTCGGAGATGGTTAGC--TATCTAACCCC	65
Db	479	TGGCTGTGATTICAGTATGATTTAGTGGCTGTTGTCGAAGGGTCCACTTCGTA	538	Qy	279	TTTGTCCGGAAACAGACAGAGTGGTGAAGGGATGATGCACTGGAAATGCTCT	338
Qy	737	ATTTGGTGGAAACTGCACAGGAGAAGCCAAATTCCCGCGCCTGATTATTGCT	796	Db	66	ATTACACAGAAGATACCGAGACTGTGGCCAGAGGCCCGCACCAATCTGAATGCTGC	125
Db	539	TGGCTGTGATTGAACTCAGGAGAATGAGCCAAATTCCCGCGCCTGATTATTGCT	598	Qy	339	CGRATGTTGCGGGTGTGGTGTCTGATGAGCTTGTGCAATGTTTCATAAATACAA	398
Qy	797	C 797		Db	126	CATCATGATCACTGTCATGTCATGACTATCCTCCTGGTGTCTGATAATACAG	185
Db	599	C 599		Qy	399	GTTTATAAAGCTTATTCTGATGGCTTATTGTGAGCASTTTTCCTCTTCTTCTATT	458
Db				Db	186	GTGCTATAAGTCATCCAGCTGCTTATATATICATCTCATGGTGTGTTCTT	245
Qy				Qy	459	CACTACAATCTATGTGCGCAGAAAGTTCTGAAAAAGTTCTGACTATT	518
LOCUS	AW850573	593 bp	mRNA	Db	246	TTCATTCATTACTTGTGGACATCATTCAT	305
DEFINITION	II.3-Ct01.9-160200-060-H03	EST	mRNA	Qy	519	GTTTTGGATGCTGGTAACTTGGAGTTCTCGAAUTGATGTTGATCATGAAAG	578
ACCESSION	AW850573	GI:7946090		Db	306	TGTGCACTCCTGTGAATTGGTGGTGGAAAGTTCATCAGTGAAG	365
VERSION	AW850573.1			Qy	579	TCCATGGCCTGGCAACAGCTTACCTTACATGCTGCTGACTAATGGCTCTGGCTT	638
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SOURCE				Qy	639	TATCAAGTACCTACCGAAATGGACTGTGCGTTGTTATCTCGTTGGGAA	698
ORGANISM	Homo sapiens			Db	426	TATCAAGTACCTCCCTGAATGGACTGCGGCTATCTGCTGATTATGTA	485
REFERENCE	1 ('bases 1 to 593)			Qy	699	TCTGTTGCGTGTACACCAAAAGGACCATGGATATTGGAAACTGGCACAGGA	758
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordim S., Costa F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			Db	486	TTTAGTGGCTGTGTTGTGTCGGAAGGTCACPTCGTATGCTGTTGAAACGCTCAGGA	545
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			Qy	759	GAGAACGCCAAATTTCGGGGCTGATTATTTCGTT	797
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			Db	546	GAGAAATGAAACGCCATTTCAGGTCATTTACTCC	584
MEDLINE	2002663			RESULT	37		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br			LOCUS	AW604231	599 bp	mRNA linear EST 23-MAR-2000
FEATURES	source	This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=gt2-IL3-Ct0219-160200-060-H03&tl3=2000-0-16&t4=1) Seq. primer: puc 18 forward High quality sequence start: 6 High quality sequence stop: 532.		DEFINITION	IL3-Ct0219-210100-059-C05		
FEATURES	source	Location/Qualifiers		ACCESSION	AW604231		
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BASE COUNT	135	a 130 g 197 t	1 others	KEYWORD			
ORIGIN				ORGANISM	Homo sapiens		
				REFERENCE	1 (bases 1 to 599)		
				AUTHORS	HCGP		
				TITLE	http://www.ludwig.org.br/ORESTES		
				COMMENT	The FAPESP/LICR Human Cancer Genome Project Unpublished (1999) Contact: Simpson A. J. G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br		
							This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=gt2-IL3-Ct0219-210100-059-C05&tl3=2000-0-16&t4=1) Seq. primer: puc 18 forward High quality sequence stop: 563.
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RESULT 50

LOCUS AW367418 553 bp mRNA linear EST 04-FEB-2000

DEFINITION MRO-HT064-211099-003-903 Homo sapiens cDNA, mRNA sequence.

VERSION AW367418

VERSION AW367418.1 GI:6872068

KEYWORDS EST.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 553)

AUTHORS HCGP http://www.ludwig.org.br/ORESTES.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999).

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpon@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/orests3/1999-10-21&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 28

High quality sequence stop: 553.

Location/Qualifiers

FEATURES

source

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Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the PUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT

ORIGIN

Query Match 12.6%; Score 189.4; DB 10; Length 553;

Best Local Similarity 61.0%; Pred. No. 2.7e-23; Matches 307; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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Db 50 GATACCGAGACTGTGGCCAGAGGCCCTGCACATTAATCTGAATCATGATC 109

Qy 349 TGCCTGGTCGTTCTGTGACAGTTCTGTGTTATAATACAGTTTATAAG 408

Db 110 AGTGTCAATTGTTGTCTGATCATGATCCCTGTGTTCTGTGTTATAAG 169

Qy 409 CCTATTCATGGATGGCTTATGTCACTGAGTTCTCTTCCTTCTTCAATCACAATC 468

Db 170 GTCATCCATGCCCTGGTTATATATCATCTCATGGTTCTGTTTTCATTATT 229

Qy 469 TATGTGCAAGAAGTTGAAAAAGTTCGATGTTGTCAGTCAGGCACATTGGTTTGGTT 528

Db 230 TACTGGGAAAGTGGGTGTTAACCTTAACCTTAACCTGCGTGGACTAATGTTGCACTC 289

Qy 529 GGACTGGTAACTATGGATCTCGAAATGATGTATACTGGAAAGGTCCATTGGGT 588

Db 290 CTGATCTGGAAATTGGGTGTTGGGAATGATTCCATTCACTGGAAAGTCCACTTCGAA 349

Qy 589 CTGCAAACAGTCTACCTTATACAATGTCGACTAATGGCTTATCAAGTAC 648

